Clean Version of Claims

1. (Thrice Amended) A method of food product testing, such method including the steps of

taking a sample of a food product, the sample including at least one unprocessed foodstuff for preparation of the food product;

preparing the food sample for assay for genomic material of a plurality of target species potentially present in the food product;

contacting the prepared food sample with an array of probes directed to multiple regions of genomic material for each of the plurality of said target species;

forming an output distribution representative of each of the plurality of target species;

storing the output distribution in a database; and

mining the database to correlate the output distribution with predictive qualitative properties,

whereby the genomic material from the plurality of target species present in the food sample selectively hybridizes to the array of probes and the output distribution of target species present is used to predict food quality and processing conditions.

2. (Once Amended) The method of claim 1, wherein the step of preparing includes the step of culturing the food sample to increase populations of a plurality of the target species prior to testing with the array of probes.

3. The method of claim 2, wherein the step of preparing includes the steps of
extracting nucleic acid from target organisms, and
labeling and amplification of gene regions prior to detection with the probe array.

4. The method of claim 3, wherein the step of labeling is performed after the step of amplification.

5. The method of claim 3, wherein the step of amplification is performed by automated fluidics and incubation to produce output material for detection by said array.

6. The method of claim 1, carried out by an automated sample preparation and array testing system.

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8. (Once Amended) The method of claim 1, wherein the step of preparing the sample includes the steps of recovering a plurality of different microorganisms from the food sample, extracting DNA from the plural different microorganisms, and simultaneously amplifying plural target sequences present in the recovered DNA for each of said different microorganisms.

9. (Once Amended) The method of claim 1, further comprising the step of correlating the output distribution with a database wherein the database includes data of at least one type selected from among

(i) other output distributions,

(ii) parameters related to the source, condition or processing of food in the sample from which the output distribution was taken, and

(iii) parameters related to the source, condition or processing of food in the sample from which other output distributions were taken.

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14. (Thrice Amended) A testing method for food quality and processing comprising the steps of

preparing an array having plurality of probes directed to target sequences of each of a defined plurality of different target species wherein the target species include species affecting quality or processing of a food product;

preparing a sample of the food product, wherein the step of preparing a sample includes extracting DNA from the sample, including sequences of the species present in the sample;

treating the extracted DNA with a PCR protocol effective to preferentially and simultaneously increase the level of target DNA sequences of the defined plurality of different target species;

hybridizing the amplified DNA to the probes on the array;

forming an output distribution representative of the plurality of target species present in the sample;

storing the output distribution in a database; and

mining the database to correlate the output distribution with predictive qualitative properties,

whereby the output distribution of target species present in the food sample can be correlated to extrinsic parameters so that predictions can be made regarding food quality and processing.

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17. The testing method of claim 14, wherein the species are foodborne species affecting food safety or quality.

C4 18. (Once Amended) The testing method of claim 14, wherein the target sequences include species sequences coding for factors involved in pathogenesis or virulence factors.

19. The testing method of claim 14, wherein the target sequences are species sequences selected for efficient PCR amplification as a group.

20. The testing method of claim 14, wherein the array tests for a palette of species selected from among product colonizing species, environment colonizing species, and mammalian colonizing species.

C5 21. (Once Amended) The testing method of claim 16, further comprising the step of displaying the distribution with a note describing adverse consequences or process warning indications associated with the detected distribution.

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23. The testing method of claim 14, wherein the target sequences are species sequences selected for efficient probe hybridization and detection as a group.

24. The testing method of claim 14, further including the steps of determining sensitivity and cross reactivity of the array.

25. The testing method of claim 14, wherein the output distribution indicates amount of each target species present in the sample.

C6 26. (NEW) The method of claim 1, wherein the qualitative properties are selected from the group comprising smell, texture, organoleptic properties, and taste.

27. (NEW) The method of claim 1, wherein the method further comprises correlating the output distribution with processing conditions.

28. (NEW) The method of claim 27, wherein processing conditions are selected from the group comprising quality and source of a component, flavor potential, and shelf-life.

29. (NEW) The testing method of claim 14, wherein the qualitative properties are selected from the group comprising smell, texture, organoleptic properties, and taste.

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30. (NEW) The testing method of claim 14, wherein the method further comprises correlating the output distribution with processing conditions.

31. (NEW) The testing method of claim 30, wherein processing conditions are selected from the group comprising quality and source of a component, flavor potential, and shelf-life.